

## Figure 1

2.

### ECTAMAGG113

#### CTAF

ALLELE 1: 1 TAAAGGGATATGGTTTCACTAATG-CCTGAAATTCAACCC-AGATTTTGCAATTtGATTttgaaaaatgt

ALLELE 2: 1 TAAAGGGATATGGTTTCACTAATGtC-GTAAAATTCAACCCaa-ATTTTTGCATTtT-----

#### CTAR

ALLELE 1: 74 tagatataATCATGTTTTACAAGCATTACAATAATTCACTCGTATATTAGGAATTc 133

ALLELE 2: 61 ATCATGTTTTACAAGCATTACAATAATTCACTCGTATATTAGGAATTc 113

### ECCGM AAC405

#### A2D8F

ALLELE1: 1 TAAAACCTGGGATGGTACAGTACGGCC-----ATCAACTAAATA-TctGCA

ALLELE2: 1 TAAAACCTGGGATGGTACAGTACGGCCAtggttttagccAACTCAACTAAATA-TGCA

ALLELE1: 62 AACGATAATAATTATAAGAAAGAC-aACCTTGAGGGCATTTTGACTTGAGAGAACTCAGGTATCAATCTAA

ALLELE2: 74 AACGATAATAATTATAAGAAAAGACT-CACTTGAGGGCATTTGACTTGAGAGAACTCAGGTATCAATCTAA

ALLELE1: 138 AACGAAACGCTGTTACCTTGAGCTGAAACACCTGGAGGAAGCAAAAGCAAACGCGAGAGAAATAAG

ALLELE2: 150 AACGAAACGCTGTTACCTTGAGCTGAAACACCTGGAGGAAGCAAAGCAAACGCGAGAGAAATAAG

ALLELE1: 214 AACGGAAACagAGAGAGAGGGACCTGTTCAAAGCAACGGGGACAACTTAGACCCCTGGCGCTGGGG  
MICROSATELLITE

ALLELE1: 291 GTCAATAAGCGTAACCTGGTGAAGGGAGCCCTGGTCAAAGCAGAAAGGAAAGAG-CaCGAGA

ALLELE2: 299 GTCAATAAGCGTAACCTGGTGAAGGGAGCCCTGGTCAAAGCAGAAAGGAAAGAGCc-CGAGA

ALLELE1: 365 CCAAGAAACACTCCTCGAAAGCAGAAAGGAATTc 397

ALLELE2: 373 CCAAGAAACACTCCTCGAAAGCAGAAAGGAATTc 405

### ECCGMAGC116

Allele 1 : 1    GAATTCCGGTTATCTGACAACCTTTGGTTGGTTATAGTAAGACACGATTAT  
Allele 2 : 1    GAATTCTGGTTATCTGACAACCTTTGGTTGGTTATAGTAAGACACGATTAT

Allele 1: 60    CCAGGCTTGGAGGGCATAGAAATAATTATTTTATATAaaaaAAAGTCTCTTAA

Allele 2: 60    CCAGGCTTGGAGGGCATAGAAATAATTATTTTATATAaaaaAAAGTCTCTTAA

### EATGMCAGC87

Allele 1 : 1    GAATTCATGGTTCTCTTAT-----GACATTGGTGCAGAAAGTAATACTACTATAAATTCAAGTTGGTTT  
Allele 2 : 1    GAATTCATGGTTCTCTTATGACATTGGTGCAGAAAGTAATACTACTATAAATTCAAGTTGGTTT

Allele 1: 68    CTGATAACCGTGGTCGTTAA 87

Allele 2: 73    CAGATAACCGTGGTCGTTAA 92

### ECCC MAGC161

Allele1: 1    TTAATGAAAATCGATCAAATCAAATATGCTTTTTAGTTGAGAATTGTTGT-GGTCAAGT-ACT  
Allele2: 1    TTAATGAAAATCGATCAAATCAAATATGCTTTTTAGTTGAGAATTGTTGT-GGTCAAGT-ACT

Allele1: 61    TTTTTTATTGAAAAATGCCAACGTTGAAACACATGTTGAGAATTGTTGT 116

Allele2: 62    TTTTTTATTGAAAATGCCAACGTTGAAACACATGTTGAGAATTGTTGT 117

Allele1: 117    GCATCCAACGTTCTCTGTACAATCAGCTGTGAGAGGGAAATTC 161

Allele2: 118    GCATCCAACGTTCTCTGTACAATCAGCTGTGAGAGGGAAATTC 162

### ECCAMAGC114

Allele1: 1    GAATTCCAGCC-AGATTTGTATCAAACATGTATGTCACAAAATGTTCAAGCATCTTA 59  
Allele2: 1    GAATTCCAG-CTAGATTGTATCAAACATGTATGTCACAAAATGTTCAAGCATCTTA 59

Allele1: 60    GGGAACTGCTTACTCTAAATTTTTATGACATCCAAGTGTGCTTTAA 114

Allele2: 60    GGGAACTGCTTACTCTAAATTTTTATGACATCCAAGTGTGCTTTAA 114

b. EATGMcGA87 BAC extension and TaqMan probe and primers

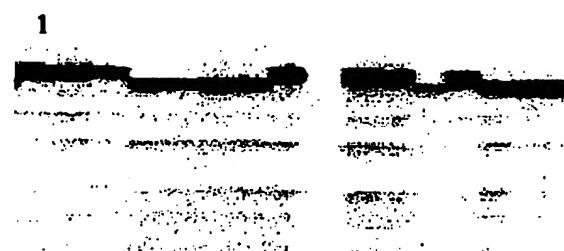
Allele 1:	ttatcatccaaaattaaaaactttaatacaaatgcacattttggaggccattcatgtc         ttatcatccaaaattaaaaactttaatacaaatgcacattttggaggccattcatgtc	<i>TMA5F</i>	atctctggctctgagcttattctgtggattgaattcatggtttctttat-----GACATGTT         atctctggctctgagcttattctgtggattgaattcatggtttctttatGACATGTT	<i>TMA5-RE</i>
Allele 1:	atctctggctctgagcttattctgtggattgaattcatggtttctttat-----GACATGTT         atctctggctctgagcttattctgtggattgaattcatggtttctttatGACATGTT	<i>TMA5R</i>	atctctggctctgagcttattctgtggattgaattcatggtttctttat-----GACATGTT         atctctggctctgagcttattctgtggattgaattcatggtttctttatGACATGTT	<i>TMA5-S</i>
Allele 1:	GCCAAGTAATACTACTATAATTCAGATTGGGTTTCTGATAACCGTGGTCGTTAataactatataatacc         GCCAAGTAATACTACTATAATTCAGATTGGGTTTCTGATAACCGTGGTCGTTAataactatataatacc		ATG4BACF	
Allele 2:				

Figure 2

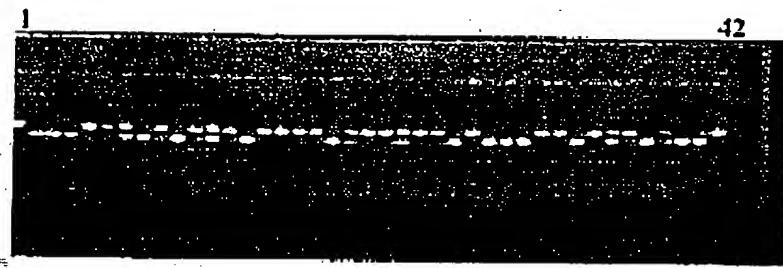
A



B



C



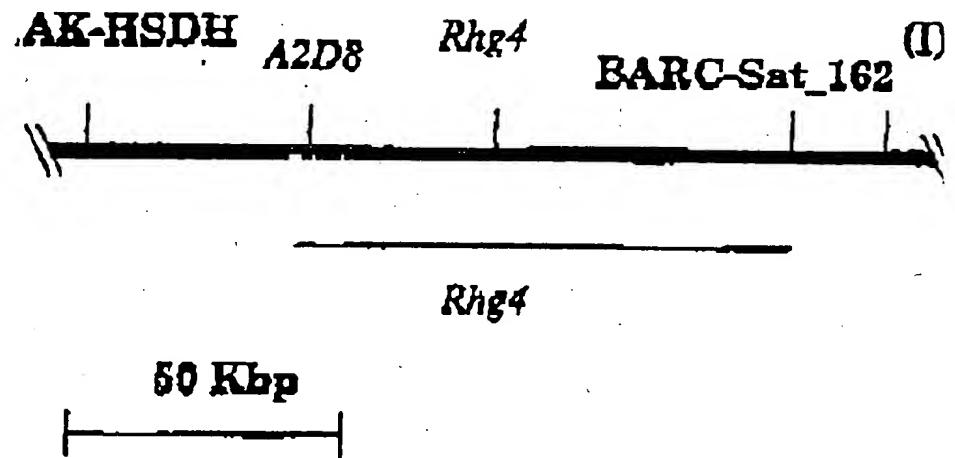
211122H1212 H 212221H22 H2212 1 11 22 12 H21H1 F E

D



2 12H11121222H2121 21 11 112122 122222 12

Figure 3



**Figure 4**

$\approx 12$  kb

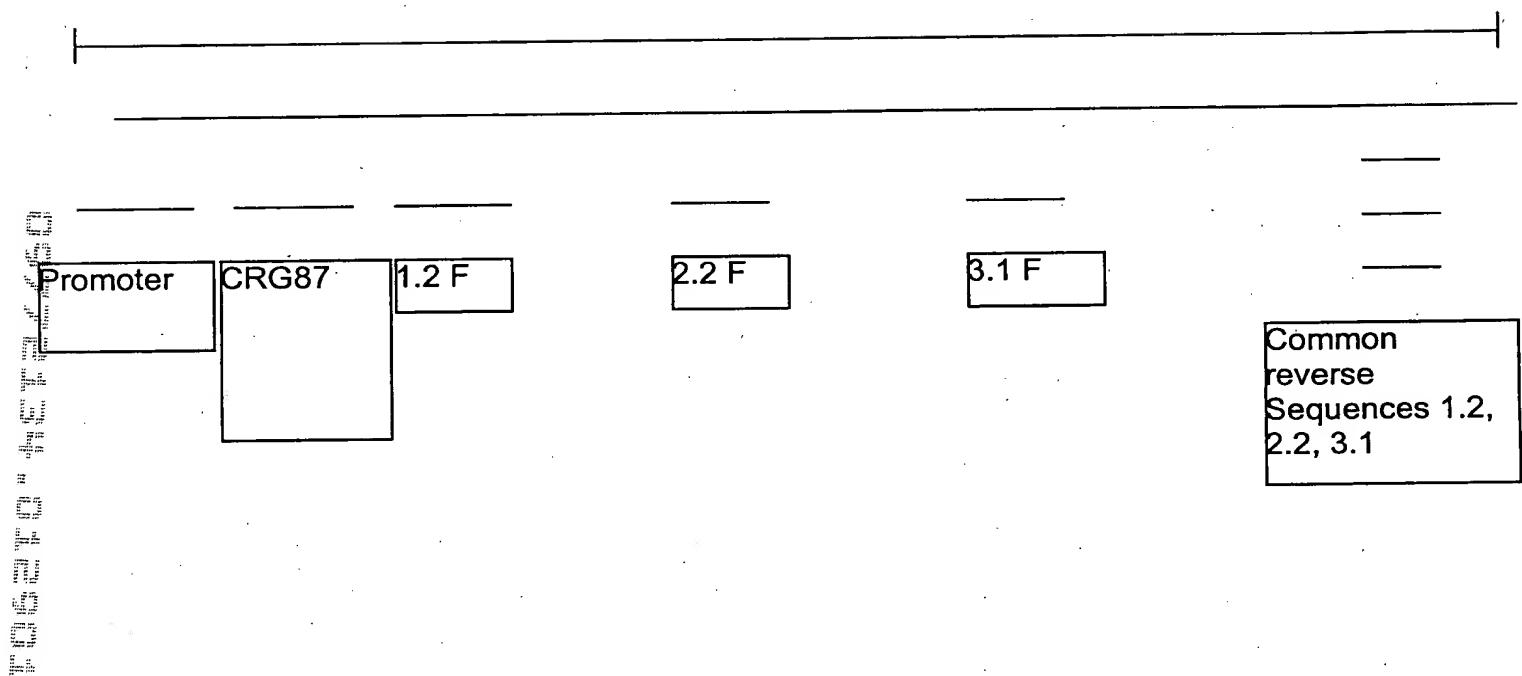


Figure 5

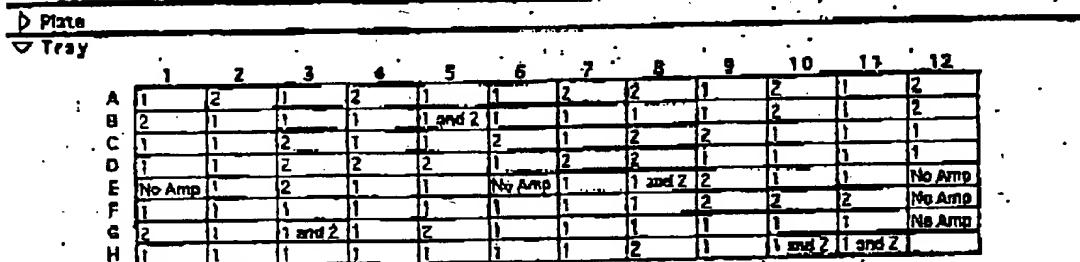
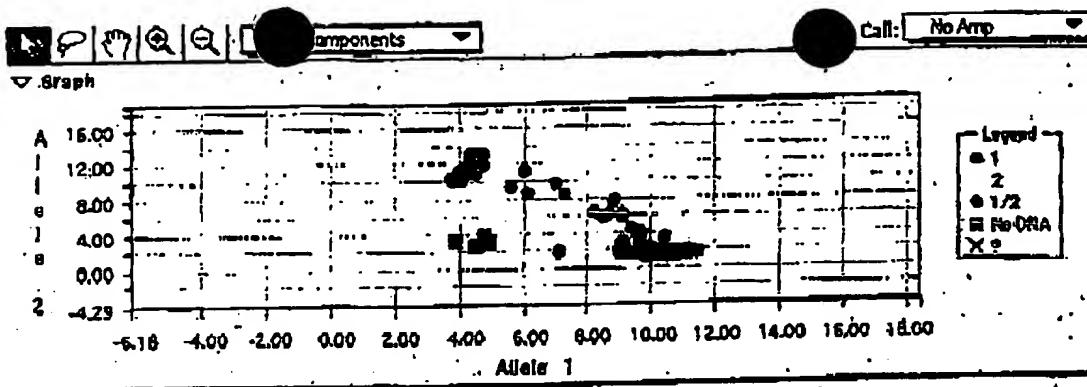


Figure 6

6

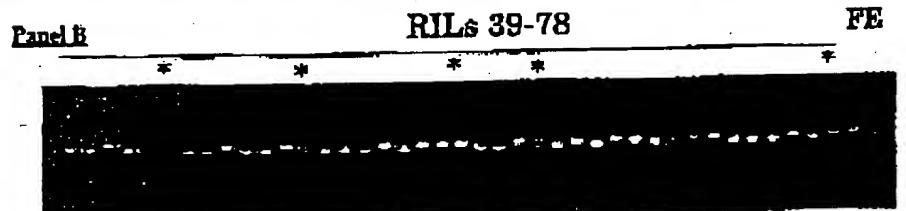
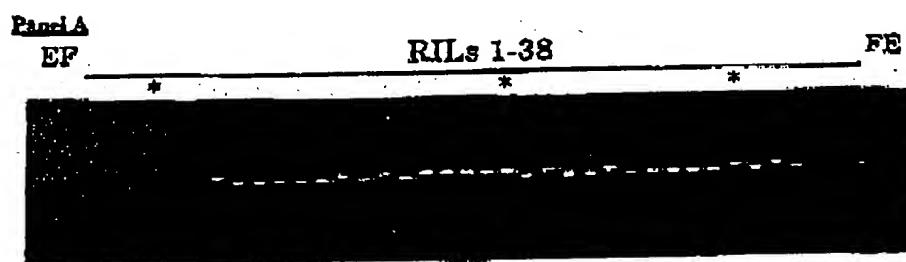


Figure 7A

Synthetic rhg1 gene

1  
AATGGGAGGAGTGGGAAAGACAGTGGCTATGGAGCCTGTTCCGGAGGTTGGGTTGGAAT  
CAAGTGTGCTCAGGGACAGGTTATTGTGATCCAGCTCCTGGAAGGGTTGAGGGGTC  
GAATCACCGACAAAATTGCCAACCTCAAGGCCTCAGGAAGCTTAGTCTTCATGATAAC  
CAAATTGGTGGTCAATCCCTCAACTTGGACTTCTTCCAACCTTAGAGGGGTTCA  
GTTATTCAACAATAGGCTTACAGGTTCCATACCTCTTCTTCTTCTTCTGCTTCTGCT  
TCAAGTCTCTGACCTCAGCAACAATTGCTCACAGGAGCAATCCCTATAGTCTTGCT  
AATTCCACTAAGCTTATTGGCTTAATTGAGTTCAACTCCTCTGGTCTTCTGCT  
AGCTAGCCTAACTCACTCATTCTCTCACTTTCTTCTTCTTCTTCTTCTGCT  
CTGGCTCCCTCCTAACTCTGGGGTGGGAATTCCAAGAAATGGCTCTTCTGCT  
AATTGATCCTAGATCATAACTTTCACTGGTGACGTTCTGCTTCTTGGTAGCTT  
AAGAGAGCTCAATGAGATTCCCTTAGTCATAATAAGTTAGTGGAGCTACCAAAATG  
AAATAGGAACCCCTTCTAGGCTTAAGACACTTGACATTCTAATAATGCCTGAATGGG  
AACTTGCGCTGCTACCCTCTCAATTATCCTCACTTACACTGCTGAATGCAGAGAACAA  
CCTCCTGACAATCAAATCCCTCAAAGTTAGGTAGATTGCGTAATCTTCTGTTCTGA  
TTTGAGTAGAAACCAATTAGTGGACATATTCCCTCAAGCATTGCAAACATTCCCTCG  
CTTAGGCAGCTGATTGTCACTGAATAATTCACTGGAGAAATTCCAGTCCTTGA  
CAGTCAGCGCAGTCTAAATCTCTCAATTGTTCTACAATAGCCTCTCAGGTCTGTCC  
CCCCTCTGCTGCCAAGAAATTAACTCAAGCTCATTGTGGAAATTCAACTATGT  
GGGTACAGCCCTCAACCCATGTCTTCCAAGCTCCATCACAAGGAGTCATTGCC  
ACCTCCTGAAGTGTCAAAACATCACCACATAGGAAGCTAACGACCAAAGACATAATTC  
TCATAGTAGCAGGAGTTCTCTCGTAGTCCTGATTACTTTGTTGTGCTGCTTTC  
TGCCTGATCAGAAAGAGATCAACATCTAGGCCGGAACGCCAACCGAGGGTAG  
AGCGGCCACTATGAGGACAGAAAAAGGAGTCCCTCAGTTGCTGGTGGTAGTTGAAG  
CAGGTGGGGAGGCTGGAGGGAAACTAGTCATTGATGGACCAATGGCTTACAGCT  
GATGATCTTTGTGTGCAACAGCTGAGATCATGGAAAGAGCACCTATGGAACTGTTA  
TAAGGCTATTGGAGGATGGAAGTCAAGTTGCAAGTAAAGAGATTGAGGGAAAGATCA  
CTAAAGGTATAGAGAATTGAATCAGAACAGTCAGTGTCTAGGAAAAATTAGACACCC  
AATGTTTGGCTCTGAGGGCCTATTACTTGGGACCAAAGGGAAAAGCTCTGGGTTT  
TGATACATGTCTAAAGGAAGTCTTGTGCTTCTTACATGGAAGGTTGCTGCTGGTT  
CTTCAATTAAAGTGTGTGCTGGTCTTAAATTATAATTGGAGTTTACCTTAGT  
AATCTGTATAATTCTAACGGAGAACAGTACAAACAAAAACACCTAACGAAACAACACCT  
TANCTTAATATACCATATCAATAAAAGTGAATATTCTGGTCATCTGATGCAGGG  
GGAACACTGAACATTCAATTGGCCACAAGATTAAATAGCCAAAGCCTTGGCCGGGCT  
TGTTGCCTCATTCCCAGGAGAACATCATACTGGACCTCNCATCCAGCAATGTGTG  
GCTTGATGAAAAACAAATGCTAAATTAGTACAGTCTTGGCTTTTGGGTTGATGTCAAC  
TGCTGCTAATTCCACAGTGATAGCTACAGCTGGAGCATTGGATACCGGGCACCTGAGCT  
CTCAAAGCTCAAGAAAGAACACTAAAACAGTATCTACAGTCTGGTGTATCTTGT  
TAGAACTCTAACGAGGAAATCACCTGGGTGTCTATGAATGGACTAGATTGCCTCAG  
TGGGTTGCCTCAGTTGTCAGGAGGAGTGGACAAATGAGGTTTGTGATGCAGACTGAT  
GAGAGATGCATCCACAGTTGGCGACGAGTTGCTAACACGTTGAAGCTCGCTTGCAC  
GTGTTGATCCTCTCCATCAGCACGACAGAGTCAAGTTCTCCAGCAGCTGAAG  
AGATTAGACCAGAGAGATCAGTCACAGCCAGTCCGGGGACGATATCGTATAGCACAAA  
TTTGCAATTGATTGGCTAAATGTAGTAGGCCTACTATATATGTTCTATGAT

Figure 7B

TCTTCATTCTTATATTATTTGCCTGTTGAATGCTTGAATTGTACATACTCATAC  
TACAATAAGGTGTAGTTCTGGTTAATTTCACCTCTACCTCAAAGCTGGGTGTAATTCT  
GTTTCCTCCAAGGCACATAATAGTTGAAAATAGTCTCAGGAGCATTCTTATTG  
TGCAAGATTCTCTTACGGCTGCTATCTCTATGCATGCCCTGCCATAAAATGCATTA  
TGAAGAATTGTAACGGCTGTGTTTGGACTTCTCAAAAAGTTATGTTATTGCCAGG  
TGTATATATCAACATGTTAAAGATTCTAAACAATCAGGTTTAGATGTGGGTTGC  
ATGCATGAGATTGGACTAGTGCCTTGATGTAGTAAAATATAAAATTGTCCAATCAAG  
CACCCCTCTACATGTCCAAATAATGGGCCTTATGAAACTTAATTCTTAATTACAAACTA  
CAGTAATCTTTGAATAAAGATTACAAATTACACNGACATGTGAAGCNGCATCTT  
NATTGNCAATCTTCAAGTTACTCTATTATTTCTGCN

3105bp

Figure 7C

Rhg1 Peptide

NGRSGKDGYGACSGGWVGIKCAQGQVIVIQLPWKGRLRGRIT  
DKIGQLQGLRKLSLHDNQIGGSIPSTLGLPNLRGVQLFNNRLG  
**SIP**  
**LSLGFCPLLQSLDLSNNLLTGAIP**  
**YSLANSTKLYWLNLNSFNSFSGPLP**  
ASLTHSFSLTFLSLQNNNLGSGLPNSWGG  
NSKNGFFRQLNLI LDHNFFTGDVP  
ASLGLSLRELNEISLSHNKFSGAIP  
NEIGTLSRLKTLDISNNALNGNLP  
ATLSNLSSLLNAENNLLDNQIP  
QSLGRLRNLSVLILSRNQFSGHIP  
SSIANISSLRQLDLSLNNFSGEIP  
VSFDSQRSLNLSNVSYNSLGSVP

PLLAKKFNSSSFVGNIQLCGYSP

STPCLSQ

APSQGVIAPPPEVSKHHHHR

**KLSTKDIILIVAGVLLVVLIILCCVLLFCLIRKRS**

TSKAGNGQATEGRAATMRTEKGVPPVAGGDVEAGGEAGGKLVHF  
DGPMAFTADDLLCATAEIMGKSTYGTVYKAILEDGSQAVKRLR  
EKITKGHREFESEVSVLGKIRHPNGLALRAYYLGPKGEKLLVFD  
YMSKGGLLFYMEGSCAGSFIKVLCVLVFNYNLEFYLSNLYNSN  
RRTVQTKTPKEQHLXFNI PYQ  
-SEIFSWSS-CRGN-TFIIGHKMKIXQDLAVACSPSFPE  
TSYMD LXSSNVCX-NXMLKLQFWFSFSVDVNCC-FQRDSYSWSIGIPGT-  
ALKAQESKH-N-YLQSWCYLVRTPNEEITWGVYEWTRFASVGCL  
SCQRGVDK-GF-CRLDERCIHSWRRVAKHVEARFALC-SFSIS  
TTRSSSSPAAGRDTREISHSQSHLPGRPLEPYSEY

Figure 7D

Sequences producing significant alignments:	Score (bits)	E Value
pir:T46070 hypothetical protein T18N14.120 - Arabidopsis thaliana	632	e-180
pir:T47727 hypothetical protein F18O21.60 - Arabidopsis thaliana	344	1e-95
pir:T04587 hypothetical protein F23E13.70 - Arabidopsis thaliana	268	9e-71
pir:T49038 hypothetical protein T5P19.20 - Arabidopsis thaliana	257	2e-67
pir:T48210 hypothetical protein T20L15.160 - Arabidopsis thaliana	241	1e-62
pir:T05050 protein kinase homolog M3E9.30 - Arabidopsis thaliana	238	2e-61
pir:T18536 receptor-like protein kinase - Ipomoea nil (Japanese...	236	3e-61
pir:T48489 receptor-like protein kinase - Arabidopsis thaliana	236	5e-61
pir:T10515 disease resistance protein Cf-2.2 - currant tomato	235	6e-61
pir:T10504 disease resistance protein Cf-2.1 - currant tomato	235	6e-61
pir:T30553 disease resistance protein Hcr2-5D - tomato	229	4e-59
pir:S27756 receptor-like protein kinase 5 (EC 2.7.1.-) precursor...	227	1e-58
pir:T48499 receptor-like protein kinase-like protein - Arabidop...	226	3e-58
pir:T46033 receptor protein kinase-like protein - Arabidopsis t...	226	4e-58
pir:T05335 hypothetical protein F1C12.190 - Arabidopsis thaliana	221	1e-56
pir:T10636 hypothetical protein T13K14.100 - Arabidopsis thaliana	219	7e-56
pir:T05898 hypothetical protein F6H11.170 - Arabidopsis thaliana	218	1e-55
pir:T45717 receptor-kinase like protein - Arabidopsis thaliana	212	7e-54
pir:T05322 hypothetical protein F18F4.240 - Arabidopsis thaliana	211	1e-53
pir:T10659 probable serine/threonine-specific protein kinase (E...	211	2e-53
pir:T03784 probable receptor protein kinase - rice	208	1e-52
pir:T50851 receptor protein kinase homolog [imported] - soybean	201	1e-50
pir:T45647 receptor protein kinase-like protein - Arabidopsis t...	199	5e-50
pir:T45718 receptor-kinase like protein - Arabidopsis thaliana	199	7e-50
pir:T50850 receptor protein kinase homolog [imported] - soybean	199	7e-50
pir:T45645 receptor kinase-like protein - Arabidopsis thaliana	196	3e-49
pir:T09356 brassinosteroid-insensitive protein BRI1 - Arabidops...	196	3e-49
pir:T00712 protein kinase homolog F22O13.7 - Arabidopsis thaliana	190	2e-47
pir:A57676 protein kinase Xa21 (EC 2.7.1.-), receptor type prec...	190	3e-47
pir:S39476 kinase-like transmembrane protein TMK11 precursor - ...	188	1e-46
pir:T02154 protein kinase homolog T1F15.2 - Arabidopsis thaliana	188	1e-46
pir:T10725 protein kinase Xa21 (EC 2.7.1.-) A1, receptor type - ...	186	5e-46
pir:T05897 protein kinase homolog F6H11.160 - Arabidopsis thaliana	184	1e-45
pir:T04313 protein kinase Xa21 (EC 2.7.1.-), receptor type - rice	183	3e-45
pir:T10727 protein kinase Xa21 (EC 2.7.1.-) D, receptor type - ...	181	2e-44

Figure 7E

>pir:T46070 hypothetical protein T18N14.120 - Arabidopsis thaliana  
Length = 836

Score = 632 bits (1613), Expect = e-180  
Identities = 329/550 (59%), Positives = 400/550 (71%), Gaps = 2/550 (0%)  
Frame = +1

Query: 7 RSGKDGYGACSGGWVGIKCAQGQVIVIQLPWKGRLRGRITDKIGQLQGLRKLSLHDNQIG 186  
+S +S GW GIKC +GQV+ IQLPWKGL G I++KIGQL LRKLSLH+N I  
Sbjct: 72 KSWNNASSQVCSCWAGIKCLRGQVVAIQLPWKGLGGTISEKIGQLGSLRKLSLHNIVIA 131

Query: 187 GSIPSTLGLLPNLRGVQLFNNRLTGSIPLSLGFCLCFKSLDLSNNLLTGAIPYSLANSTK 366  
GS+P +LG L +LRGV LFNNRL+GSIP+SLG C ++LDLS+N LTGAIP SL ST+  
Sbjct: 132 GSVPRSLGYLKSLRGVYLFNNRLSGSIPVSLGNCPPLLQNLDLSSNQLTGAIPPSLTESTR 191

Query: 367 LYWLNLNFNSFSGPLPASLTHFSLTFLSLQNNNLSGSLPNWGGNSKNGFFRLQNLILD 546  
LY LNLSFNS SGPLP S+ S++LTFL LQ+NNLSSGSP+ + NG L+ L LD  
Sbjct: 192 LYRLNLNFNSLGPLPVSVARSYTLTFLDLQHNNLNGSIPDFF----VNGSHPLKTLNLD 247

Query: 547 HNFFTGDVPASLGSRELNEISLSHNKFGAIPNEIGTLSRLKTLDISNNALNGNLPATL 726  
HN F+G VP SL L E+S+SHN+ SG+IP E G L L++LD S N++NG +P +  
Sbjct: 248 HNRFSGAVPVSLCKHSLLVEVSIHNQLSGSIPRECGGLPHLQSLDFSYNSINGTIPDSF 307

Query: 727 SNLSSLTLLNAENNLLDNQIPQSLGRLRNLSVLILSRNQFSGHIPSSIANISSLRQLDLS 906  
SNLSSL LN E+N L IP ++ RL NL+ L L RN+ +G IP +I NIS +++LDLS  
Sbjct: 308 SNLSSLVSLNLESNHLKGPIPDADRLHNLTELNLKRNKINGPIPETIGNISGIKKLDLS 367

Query: 907 LNNFSGEIPVSFDSQRSLNLFNVSYNSLSGSVPPLLAKKFNSSSFVGNIQLCGYSPSTPC 1086  
NNF+G IP+S L+ FNVSYN+LSG VPP+L+KKFNSSSF+GNIQLCGYS S PC  
Sbjct: 368 ENNFTGPIPLSLVHLAKLSSFNVSYNTLSGPVPPVLSKKFNSSFLGNIQLCGYSSSNPC 427

Query: 1087 LSQAPSQGVIAPP--PEVSKHHHRKLSTKDIILIVAGVLLVVLIILCCVLLFCLIRKRS 1260  
+ + P + + HHHRKLS KD+ILI G LL +L++LCC+LL CLI+KR+  
Sbjct: 428 PAPDHHPPLTLSPTSSQEPRKHHHRKLSVKDVILIAIGALLAIIILLCILLCCLIKRA 487

Query: 1261 TSRPGTAKPPEGRAATMRTEKGVPPVAGGDVEAGGEAGGKLVHFDGPMFTAADDLLCATA 1440  
K +G+ T +EK V G AGGE GGKLVHFDGP FTADDLLCATA  
Sbjct: 488 ----ALKQKDGDKDT--SEKTVSAGVAGTASAGGEMGGKLVHFDGPFVFTADDLLCATA 540

Query: 1441 EIMGKSTYGTVYKAILEDGSQAVKRLREKITKGHREFESEVSVLGKIRHPNVLALRAYY 1620  
EIMGKSTYGT YKA LEDG++VAVKRLREK TKG +EFE EV+ LGKIRH N+LALRAYY  
Sbjct: 541 EIMGKSTYGTAYKATLEDGNEAVKRLREKTTKGVKEFEGEVTALGKIRHQNLALRAYY 600

Query: 1621 LGPKGEKLLGFD 1656  
LGPKGEKLL FD  
Sbjct: 601 LGPKGEKLLVFD 612

Figure 7F

Score = 185 bits (464), Expect = 1e-45  
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Frame = +2

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GL LHS EN+IH + ++ ++ N+ D+GL R+ + + ++GYR  
Sbjct: 647 GLAHLHSNENMIH--ENLTASNILLDEQTNNAHIADYGLSRLMTAAAATNVIATAGTLGYR 704

Query: 2114 APELSKLKKANTKTDIYSLGVILLELLTRKSPGVSMNGLDLPQWVASVVKEEWTNEVFDA 2293  
APE SK+K A+ KTD+YSLG+I+LELLT KSPG NG+DLPQWVAS+VKEEWTNEVFD  
Sbjct: 705 APEFSKIKNASAKTDVYSLGIIILELLTGKSPGEPTNGMDLPQWVASIVKEEWTNEVFDL 764

Query: 2294 DLMRDASTVGDELLNTLKLALHCVDPSPSARPEVHQVLQQLKRL 2425  
+LMR+ +VGDELLNTLKLALHCVDPSP+ARPE +QV++QL+ +  
Sbjct: 765 ELMRETQSVGDELLNTLKLALHCVDPSPAARPEANQVVEQLEEI 808